Cox2W56R complemented strain led to full restoration of Cox1 synthesis. We conclude that the cytosol-synthesized Cox2W56R follows a rate-limiting process of import, maturation or assembly that yields lower steady-state levels of complex IV. Still, the allotopically-expressed Cox2W56R restores CcO activity and allows mitochondrial Cox1 synthesis to advance at WT levels.

**References**

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## 14P9

### Modeling the circular dichroism and absorption spectra of complexes FI and FII of cytochrome *c* oxidase

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Cytochrome *c* oxidase is the key enzyme of mitochondrial and some bacterial respiratory chains. As a redox enzyme, cytochrome oxidase has several redox components, namely, hemes *a* and $a_3$ and copper centers $Cu_A$ and $Cu_B$. Intermediates of the working cycle can differ in the redox state of these centers. So the important task is to characterize the redox centers in different intermediates of the enzyme. During the peroxidase phase of the working cycle, after the heterolytic OO bond cleavage, a ferryl ($Fe^{4+}$) intermediate is formed, containing an organic radical at the active site, which is presumably represented by neutral tyrosyl radical (complex FI). After that the next electron reduces this complex to the ferryl intermediate which contain no amino acid radical at the active site (complex FII). Complex FI was obtained by bubbling oxidized enzyme with CO under aerobic conditions, complex FII was obtained by adding access amount of hydrogen peroxide to the oxidized enzyme. The absorption spectra of the two complexes clearly differ in the visible region, but in the Soret region the difference is not so distinct because of wide absorption bands. Circular dichroism (CD) spectra in the Soret region revealed narrow bands for these ferryl complexes and the distinct difference between them. However, it is difficult to interpret the spectra without theoretical considerations. To solve this task, we suggest a model [1] based on the DeVoe's theory of classical dipole oscillators. With this model in hand, we are able to simulate the spectra of oxidized and reduced states of cytochrome oxidase, and also the spectrum of complex FII, according to the 3D structure of the enzyme and the redox state of the hemes and nearby amino acid radicals. Our model have shown that the changing of optical properties of Tyr244 (bovine notation), simulating the transition to the radical state, affects the shape of the calculated CD spectra in a manner similar to the difference between spectra of complexes FI and FII.

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## 14P10

### Heme-copper terminal oxidase using both cytochrome *c* and ubiquinol as electron donors

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The cytochrome *c* oxidase Cox2 has been purified from native membranes of the hyperthermophilic eubacterium *Aquifex aeolicus*. It is a cytochrome $ba_3$ oxidase belonging to the family B of the heme-copper containing terminal oxidases. It consists of three subunits, subunit I (CoxA2, 63.9 kDa), subunit II (CoxB2, 16.8 kDa), and an additional subunit IIa of 5.2 kDa. Surprisingly it is able to oxidize both reduced cytochrome *c* and ubiquinol in a cyanide sensitive manner. Cox2 is part of a respiratory chain supercomplex. This supercomplex contains the fully assembled cytochrome $bc_1$ complex and Cox2. Although direct ubiquinol oxidation by Cox2 conserves less energy than ubiquinol oxidation by the cytochrome $bc_1$ complex followed by cytochrome *c* oxidation by a cytochrome *c* oxidase, ubiquinol oxidation by Cox2 is of advantage when all ubiquinone would be completely reduced to ubiquinol, e.g., by the sulfide:quinone oxidoreductase, because the cytochrome $bc_1$ complex requires the presence of ubiquinone to function according to the Q-cycle mechanism. In the case that all ubiquinone has been reduced to ubiquinol its reoxidation by Cox2 will enable the cytochrome $bc_1$ complex to resume working.

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## 14P11

### The heme-copper oxidoreductase superfamily: Diversity, evolution and ecology

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The heme-copper oxidoreductase superfamily is extremely diverse with members playing crucial roles in both aerobic and anaerobic respiration. The superfamily is currently divided into two classes: the oxygen reductases and the nitric oxide reductases. The oxygen reductase members of the superfamily are terminal oxidases in the aerobic respiratory chains of mitochondria and many Archaea and Bacteria. These enzymes catalyze the reduction of molecular oxygen to water with the concomitant transfer of protons across the membrane, contributing to the generation of a proton electrochemical gradient that